

38-21(52806)B Sequence Listing.txt  
 SEQUENCE LISTING

<110> Monsanto Technology LLC

Baum, James A.  
 Donovan, Judith C.

Donovan, William P.

Engleman, James T.

Krasomil-Osterfeld, Karina

Pitkin, John W.

Roberts, James K.

<120> Insecticidal Proteins Secreted From Bacillus Thuringiensis and Uses Therefor

<130> 38-21(52806)B

<150> PCT/US04/21692

<151> 2004-07-06

<150> US 60/485,483

<151> 2003-07-07

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 15

<212> PRT

<213> Bacillus thuringiensis

<400> 1

Val	Ile	Gly	Pro	Tyr	Ala	Glu	Ser	Tyr	Ile	Asp	Arg	Val	Gln	Asp
1				5					10				15	

<210> 2

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

## 38-21(52806)B Sequence Listing.txt

```

<223>  tic gene probe encoding SEQ ID NO 1

<400>  2
gtaattggac catatgcaga atcatatatt gatacgagta caaga          45

<210>  3
<211>  1253
<212>  DNA
<213>  Bacillus thuringiensis

<220>
<221>  CDS
<222>  (153)..(1253)
<223>

<400>  3
aattatgatt ttaatatctt tatgtttattc ctataatata caataaaagc ataattatcc      60
ttcatattat gtttataaat ttaataaaaat acataaaaat agagtgttat aatatttttg      120
aaagcgttat caagagtgat ggagggataa tt atg aaa aat aga ttt tca aaa      173
                                   Met Lys Asn Arg Phe Ser Lys
                                   1          5

gtg gca tta tgc acc gta ccg att tta atg gtt tct aca ttc gcc agt      221
Val Ala Leu Cys Thr Val Pro Ile Leu Met Val Ser Thr Phe Ala Ser
      10          15          20

tca agc atg tca gct ttt gct gca gaa gcc aaa tca cca gat tta aat      269
Ser Ser Met Ser Ala Phe Ala Ala Glu Ala Lys Ser Pro Asp Leu Asn
      25          30          35

gta tct caa caa gta ata ggt ccc tat gcc gaa tct tat att gat att      317
Val Ser Gln Gln Val Ile Gly Pro Tyr Ala Glu Ser Tyr Ile Asp Ile
      40          45          50          55

gtg cag gat aga atg aaa caa agg gat aag gga tca aaa tta act ggt      365
Val Gln Asp Arg Met Lys Gln Arg Asp Lys Gly Ser Lys Leu Thr Gly
      60          65          70

aaa cca ata aat atg caa gaa caa ata ata gat ggg tgg ttt cta gct      413
Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala
      75          80          85

aga ttt tgg ata ttt aag gat caa aac aat aac cat cag aca aat aga      461
Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Asn His Gln Thr Asn Arg
      90          95          100

ttt ata tcc tgg ttt aaa gat aat att gct agt tca aaa ggg tat aat      509
Phe Ile Ser Trp Phe Lys Asp Asn Ile Ala Ser Ser Lys Gly Tyr Asn
      105          110          115

agt att gcg gag caa atg ggt tta aaa ata gaa gca gaa aac gat atg      557
Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala Glu Asn Asp Met
      120          125          130          135

gat gta aca aat ata gat tat aca tct aag aca ggc gat acc att tat      605
Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp Thr Ile Tyr
      140          145          150

aat ggt att tca gaa ttg aaa aat tat aca gga tca act caa aag atg      653
Asn Gly Ile Ser Glu Leu Lys Asn Tyr Thr Gly Ser Thr Gln Lys Met

```

## 38-21(52806)B Sequence Listing.txt

155	160	165	
aaa aca gat agt ttt caa aga gat tat aca aaa tca gaa tct act tca			701
Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Glu Ser Thr Ser			
170	175	180	
gta act aat gga tta caa tta gga ttt aaa gtt gct gct aaa gga gta			749
Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala Ala Lys Gly Val			
185	190	195	
gtt gct ttg gct ggg gca gac ttt gaa acc agt gtt act tat aat cta			797
Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val Thr Tyr Asn Leu			
200	205	210	215
tca act act aca act gaa aca aat aca ata tca gac aag ttt act gtc			845
Ser Thr Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp Lys Phe Thr Val			
220	225	230	
cca tct caa gaa gtt aca ttg cct cca gga cat aaa gcg ata gtg aaa			893
Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys Ala Ile Val Lys			
235	240	245	
cat gat tta aga aaa atg gtt tat tct ggt act cat gat cta aag ggt			941
His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp Leu Lys Gly			
250	255	260	
gat tta att gtg agt ttt aat gat aaa gag att gta caa aaa ttt att			989
Asp Leu Ile Val Ser Phe Asn Asp Lys Glu Ile Val Gln Lys Phe Ile			
265	270	275	
tat cca aat tat aga gaa att aat tta tct gat atc cgt gaa act atg			1037
Tyr Pro Asn Tyr Arg Glu Ile Asn Leu Ser Asp Ile Arg Glu Thr Met			
280	285	290	295
att gaa att gat gaa tgg aat cat gta aac cct gtg aat ttt tat gaa			1085
Ile Glu Ile Asp Glu Trp Asn His Val Asn Pro Val Asn Phe Tyr Glu			
300	305	310	
tta gtt ggg gtc aaa aat cat ata aaa aat ggt gaa act ttg tat ata			1133
Leu Val Gly Val Lys Asn His Ile Lys Asn Gly Glu Thr Leu Tyr Ile			
315	320	325	
gat act cca gct aaa ttt atg ttt aat ggt gct aat cca tat tat aga			1181
Asp Thr Pro Ala Lys Phe Met Phe Asn Gly Ala Asn Pro Tyr Tyr Arg			
330	335	340	
gca aca ttt aca gaa tac gac ggg aat aat aat cct gtt caa aca aag			1229
Ala Thr Phe Thr Glu Tyr Asp Gly Asn Asn Asn Pro Val Gln Thr Lys			
345	350	355	
gta tta agt gaa aac ttt aaa ttg			1253
Val Leu Ser Glu Asn Phe Lys Leu			
360	365		

&lt;210&gt; 4

&lt;211&gt; 367

&lt;212&gt; PRT

&lt;213&gt; Bacillus thuringiensis

&lt;400&gt; 4

Met	Lys	Asn	Arg	Phe	Ser	Lys	Val	Ala	Leu	Cys	Thr	Val	Pro	Ile	Leu
1				5					10					15	

Met	Val	Ser	Thr	Phe	Ala	Ser	Ser	Ser	Met	Ser	Ala	Phe	Ala	Ala	Glu
			20					25					30		

38-21(52806)B Sequence Listing.txt

Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr  
35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp  
50 55 60

Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile  
100 105 110

Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys  
115 120 125

Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser  
130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr  
145 150 155 160

Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr  
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro  
225 230 235 240

Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser  
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys  
260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Glu Ile Asn Leu  
275 280 285

Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val  
290 295 300

Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys  
305 310 315 320

Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn

325

Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn  
340 345 350

Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu  
355 360 365

<210> 5

<211> 1621

<212> DNA

<213> *Bacillus thuringiensis*

<220>

<221> CDS

<222> (530)..(1621)

<223>

<400> 5

actagttttt tcataatggc ataagcggga tgatgatctt gttttttacg atgttcaata 60  
tccaatgtgt gccttttctat atcaatcgca cgaataaat aacactatct ccctttgaat 120  
tttatatagg ttctcatctaa ttttcaagac atgtggttgt tttgcgtttt cttcttccaa 180  
atattgataaa tcaagctccc atattcatga atccagcgca taatgattgt gggatgaact 240  
gaaacatcac gatagcttaa agcaaacgca caatagtagc ggacggctac cataataata 300  
tcttggttga actgtttccc tttaaaatat cacatttgtg attctcctcg atgctttttt 360  
tagagtgtag cttcatctag aacactttgc aatagaacca ttcctttgat atacaattaa 420  
accacattta tccttcatgg aatgtttata tattaaagaa tataaaaaaa catacgatgt 480  
tataattaat ttgaaagcgt taacaaaaat gaatgatgga gggataatt atg aaa tac 538  
Met Lys Tyr  
1

aag ttt tca aaa gtc gtt aag tgt act tta cca gct tta atg att act 586  
Lys Phe Ser Lys Val Val Lys Cys Thr Leu Pro Ala Leu Met Ile Thr  
5 10 15

aca ttc gtt act cca agt atg gca gtt ttt gcc gca gaa acc aag tcg 634  
Thr Phe Val Thr Pro Ser Met Ala Val Phe Ala Ala Glu Thr Lys Ser  
20 25 30 35

cca aat cta aat gca tct caa caa gca ata act cca tat gct gaa tct 682  
Pro Asn Leu Asn Ala Ser Gln Gln Ala Ile Thr Pro Tyr Ala Glu Ser  
40 45 50

tat att gat act gtt caa gat aga atg aaa caa aga gat agg gaa tca 730  
Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp Arg Glu Ser  
55 60 65

aaa cta act ggt aaa cca ata aat atg caa gaa caa ata ata gat gga 778  
Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly  
70 75 80

tgg ttt tta gct aga ttc tgg ata ttt aaa gat caa aat aac aat cat 826  
Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Asn His

## 38-21(52806)B Sequence Listing.txt

85	90	95	
caa aca aat aga ttt ata tcc tgg ttt aaa gat aat ctt gct agt tcg			874
Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu Ala Ser Ser			
100	105	110	115
aag ggg tat gac agt ata gca gaa caa atg ggc tta aaa ata gaa gca			922
Lys Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala			
	120	125	130
tta aat gat atg gat gta aca aat att gat tat aca tct aaa aca ggt			970
Leu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly			
	135	140	145
gat acc ata tat aat gga att tct gaa cta aca aat tat aca gga aca			1018
Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Thr Asn Tyr Thr Gly Thr			
	150	155	160
acc caa aaa atg aaa acc gat agt ttt caa aga gat tat aca aaa tct			1066
Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser			
	165	170	175
gaa tcc act tca gta aca aat ggg tta caa tta gga ttt aaa gtt gct			1114
Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala			
	180	185	190
gct aag gga gta gtt gca tta gca ggt gca gat ttt gaa aca agt gtt			1162
Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val			
	200	205	210
acc tat aat tta tca tct act aca act gaa aca aat aca ata tcg gat			1210
Thr Tyr Asn Leu Ser Ser Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp			
	215	220	225
aag ttt act gtt cca tct caa gaa gtt aca tta tcc cca gga cat aaa			1258
Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ser Pro Gly His Lys			
	230	235	240
gca gtg gtg aaa cat gat ttg aga aaa atg gtg tat ttt ggg act cat			1306
Ala Val Val Lys His Asp Leu Arg Lys Met Val Tyr Phe Gly Thr His			
	245	250	255
gat tta aag ggt gat tta aaa gta ggt ttt aat gat aaa gag att gta			1354
Asp Leu Lys Gly Asp Leu Lys Val Gly Phe Asn Asp Lys Glu Ile Val			
	260	265	270
caa aaa ttt att tat cca aat tat aga tca att gat tta tct gat att			1402
Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asp Leu Ser Asp Ile			
	280	285	290
cgt aaa aca atg att gaa att gat aaa tgg aat cat gta aat acc att			1450
Arg Lys Thr Met Ile Glu Ile Asp Lys Trp Asn His Val Asn Thr Ile			
	295	300	305
gac ttt tat caa tta gtt gga gtt aaa aat cat ata aaa aat ggt gat			1498
Asp Phe Tyr Gln Leu Val Gly Val Lys Asn His Ile Lys Asn Gly Asp			
	310	315	320
act tta tat ata gat acc ccg gcc gaa ttt aca ttt aat gga gct aat			1546
Thr Leu Tyr Ile Asp Thr Pro Ala Glu Phe Thr Phe Asn Gly Ala Asn			
	325	330	335
cca tat tat aga gca aca ttt aca gaa tac gac gag aac gga aat cct			1594
Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Glu Asn Gly Asn Pro			
	340	345	350
ggt caa aca aag att tta agt gga aat			1621
Val Gln Thr Lys Ile Leu Ser Gly Asn			
	360		

&lt;210&gt; 6

&lt;211&gt; 364

## 38-21(52806)B Sequence Listing.txt

&lt;212&gt; PRT

<213> *Bacillus thuringiensis*

&lt;400&gt; 6

Met Lys Tyr Lys Phe Ser Lys Val Val Lys Cys Thr Leu Pro Ala Leu  
 1 5 10 15

Met Ile Thr Thr Phe Val Thr Pro Ser Met Ala Val Phe Ala Ala Glu  
 20 25 30

Thr Lys Ser Pro Asn Leu Asn Ala Ser Gln Gln Ala Ile Thr Pro Tyr  
 35 40 45

Ala Glu Ser Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp  
 50 55 60

Arg Glu Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
 85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu  
 100 105 110

Ala Ser Ser Lys Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys  
 115 120 125

Ile Glu Ala Leu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser  
 130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Thr Asn Tyr  
 145 150 155 160

Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
 165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe  
 180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu  
 195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Thr Thr Glu Thr Asn Thr  
 210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ser Pro  
 225 230 235 240

Gly His Lys Ala Val Val Lys His Asp Leu Arg Lys Met Val Tyr Phe  
 245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val Gly Phe Asn Asp Lys  
 Page 7

260

265

270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asp Leu  
 275 280 285

Ser Asp Ile Arg Lys Thr Met Ile Glu Ile Asp Lys Trp Asn His Val  
 290 295 300

Asn Thr Ile Asp Phe Tyr Gln Leu Val Gly Val Lys Asn His Ile Lys  
 305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Asp Thr Pro Ala Glu Phe Thr Phe Asn  
 325 330 335

Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Glu Asn  
 340 345 350

Gly Asn Pro Val Gln Thr Lys Ile Leu Ser Gly Asn  
 355 360

<210> 7

<211> 1552

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (169)..(1272)

<223>

<400> 7

ctagctgaat atgcagtaga taatgatttt gactatacta atgagatttt ttatgtaata 60  
 aaccatattt atccttaaat aaatgttcac atatttaaaa agaataaact accatgcggt 120  
 gctagaatat aaatgagagc gctaacaaaa aataatggag ggataatc atg aaa tac 177  
 Met Lys Tyr  
 1

aaa tca tca aaa gta gca ata tgt act tta tca gct tta atg ctt tca 225  
 Lys Ser Ser Lys Val Ala Ile Cys Thr Leu Ser Ala Leu Met Leu Ser  
 5 10 15

aca att ggt act tcg agt atg tcc act ttt gct gca gaa aca aca tta 273  
 Thr Ile Gly Thr Ser Ser Met Ser Thr Phe Ala Ala Glu Thr Thr Leu  
 20 25 30 35

cca ggt caa act ctt aag gaa caa tca ata acc cca cgt gca gaa tct 321  
 Pro Gly Gln Thr Leu Lys Glu Gln Ser Ile Thr Pro Arg Ala Glu Ser  
 40 45 50

tat att gat att gta caa gat aga atg aaa caa agg gat ata gaa tcg 369  
 Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp Ile Glu Ser  
 55 60 65

aaa cgt act ggt aaa ccg att aat atg caa gaa caa ata ata gat gga 417  
 Lys Arg Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly



38-21(52806)B Sequence Listing.txt

70	75	80	
tgg ttt tta gca aga ttc tgg ata ttt aaa gat caa aat aat aac cat			465
Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Asn His			
85	90	95	
caa aca aat aga ttc ata aca tgg ttt aaa aat aat gtt gcc agc tca			513
Gln Thr Asn Arg Phe Ile Thr Trp Phe Lys Asn Asn Val Ala Ser Ser			
100	105	110	115
aaa ggt tat gag ggt att gca gaa caa atg ggt ttg aaa ata gaa tcg			561
Lys Gly Tyr Glu Gly Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ser			
120	125	130	
atg agt gat atg aat gta tcg aat ata aat tat aca ggt aaa aag ggt			609
Met Ser Asp Met Asn Val Ser Asn Ile Asn Tyr Thr Gly Lys Lys Gly			
135	140	145	
gat act ata tat aat ggc gtt tcg gaa tta gaa aat aaa atg gga aca			657
Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Glu Asn Lys Met Gly Thr			
150	155	160	
cct caa aaa atg aaa tca gat agt ttt caa aga gat tat acc aaa tct			705
Pro Gln Lys Met Lys Ser Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser			
165	170	175	
caa tca acc tca gta aca aat ggg tta caa tta gga gtt aaa gtt tct			753
Gln Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Val Lys Val Ser			
180	185	190	195
gcc aaa ggt acg gtt gtc tta gga gag gca agc ctt gaa aca agc gtt			801
Ala Lys Gly Thr Val Val Leu Gly Glu Ala Ser Leu Glu Thr Ser Val			
200	205	210	
act tat aat tta tcg tct act gca act gaa aca gat aca aca tcg gac			849
Thr Tyr Asn Leu Ser Ser Thr Ala Thr Glu Thr Asp Thr Thr Ser Asp			
215	220	225	
aag ttt act gtc cca tcc caa gaa gtt aca tta cca cca gga cat aaa			897
Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys			
230	235	240	
gca gta att aag cat gat tta aga aaa atg gtg tat tct ggt acg cat			945
Ala Val Ile Lys His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His			
245	250	255	
gac tta aag ggg gat tta aaa gta gct ttt aac gat aaa gca att gta			993
Asp Leu Lys Gly Asp Leu Lys Val Ala Phe Asn Asp Lys Ala Ile Val			
260	265	270	275
caa aaa ttt att tat cca aat tat aga tct ata aat tta tct gat att			1041
Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asn Leu Ser Asp Ile			
280	285	290	
cgt aaa aca atg aaa gaa att gat gaa tgg aat cat gta aaa ccc att			1089
Arg Lys Thr Met Lys Glu Ile Asp Glu Trp Asn His Val Lys Pro Ile			
295	300	305	
gat ttt tat caa ctg gtt gga ata aaa aat cat ata aaa aat ggg gat			1137
Asp Phe Tyr Gln Leu Val Gly Ile Lys Asn His Ile Lys Asn Gly Asp			
310	315	320	
acc tta tat ata gag act cca gct aaa ttt att ttt aat gga gct aat			1185
Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Ile Phe Asn Gly Ala Asn			
325	330	335	
gta tat tat aga gca act ttt aca gaa tat gat aag gat gga aaa cct			1233
Val Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Lys Asp Gly Lys Pro			
340	345	350	355
gtt caa ttc aac aaa ttt tta agt gaa aat tac aag tta tagaggaagt			1282
Val Gln Phe Asn Lys Phe Leu Ser Glu Asn Tyr Lys Leu			
360	365		

38-21(52806)B Sequence Listing.txt

aaagatgccg tagtgagatc gtttcacagc tactgagtat tcaaataata cacgggaaaa 1342  
 ttcaccttcc tggaaggacg gatttacttt ttttacggag gaacttggtt tatacatcaa 1402  
 aatgtttttt tatgaggttt gtgtattctt atttgagcct ggaacggaac cattttgagt 1462  
 aagcttaatt tgacttggaa atgtattttt attaccttat tacgtgaaca atggcctata 1522  
 aacgtgccac acaggaatgg gaggacgagt 1552

<210> 8

<211> 368

<212> PRT

<213> Bacillus thuringiensis

<400> 8

Met Lys Tyr Lys Ser Ser Lys Val Ala Ile Cys Thr Leu Ser Ala Leu  
 1 5 10 15

Met Leu Ser Thr Ile Gly Thr Ser Ser Met Ser Thr Phe Ala Ala Glu  
 20 25 30

Thr Thr Leu Pro Gly Gln Thr Leu Lys Glu Gln Ser Ile Thr Pro Arg  
 35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp  
 50 55 60

Ile Glu Ser Lys Arg Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
 85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Thr Trp Phe Lys Asn Asn Val  
 100 105 110

Ala Ser Ser Lys Gly Tyr Glu Gly Ile Ala Glu Gln Met Gly Leu Lys  
 115 120 125

Ile Glu Ser Met Ser Asp Met Asn Val Ser Asn Ile Asn Tyr Thr Gly  
 130 135 140

Lys Lys Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Glu Asn Lys  
 145 150 155 160

Met Gly Thr Pro Gln Lys Met Lys Ser Asp Ser Phe Gln Arg Asp Tyr  
 165 170 175

Thr Lys Ser Gln Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Val  
 180 185 190

Lys Val Ser Ala Lys Gly Thr Val Val Leu Gly Glu Ala Ser Leu Glu  
 195 200 205

38-21(52806)B Sequence Listing.txt

Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Ala Thr Glu Thr Asp Thr  
210 215 220

Thr Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro  
225 230 235 240

Gly His Lys Ala Val Ile Lys His Asp Leu Arg Lys Met Val Tyr Ser  
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val Ala Phe Asn Asp Lys  
260 265 270

Ala Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asn Leu  
275 280 285

Ser Asp Ile Arg Lys Thr Met Lys Glu Ile Asp Glu Trp Asn His Val  
290 295 300

Lys Pro Ile Asp Phe Tyr Gln Leu Val Gly Ile Lys Asn His Ile Lys  
305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Ile Phe Asn  
325 330 335

Gly Ala Asn Val Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Lys Asp  
340 345 350

Gly Lys Pro Val Gln Phe Asn Lys Phe Leu Ser Glu Asn Tyr Lys Leu  
355 360 365

<210> 9

<211> 1378

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (215)..(1306)

<223>

<400> 9  
cagtg gatag gaatttg ttt tcgtgctagg tatcaattta atttg tttcta taagataagt 60

gaagtacgat caaaatgaat acttttg tgtg attagatcaa taggtaaaat aataataaat 120

tttatatttg aaccttaaaa aattatttaa tcaaatcttt ttcactttaa aaacaaaata 180

tccagaaaaa acaatagtta acggagggat aata atg aaa tac aag tca tca aaa 235  
Met Lys Tyr Lys Ser Ser Lys  
1 5

gta gca atg tgt aca tta tca gct tta atg ctt tcg aca atc gcc act 283  
Val Ala Met Cys Thr Leu Ser Ala Leu Met Leu Ser Thr Ile Ala Thr

## 38-21(52806)B Sequence Listing.txt

10	15	20	
cca agt ata tct gtt ttc gct gca gaa aca act tcg tca cat gcg gtt			331
Pro Ser Ile Ser Val Phe Ala Ala Glu Thr Thr Ser Ser His Ala Val			
25	30	35	
act aat cag caa aca att acg cag cgt gca gaa tct tat att gat att			379
Thr Asn Gln Gln Thr Ile Thr Gln Arg Ala Glu Ser Tyr Ile Asp Ile			
40	45	50	55
gtg cac aat aga atg aaa caa aga gat att gaa tca aaa atg aca ggt			427
Val His Asn Arg Met Lys Gln Arg Asp Ile Glu Ser Lys Met Thr Gly			
	60	65	70
aaa tcc att aat atg caa gaa caa ata att gat gga tgg ttt tta gct			475
Lys Ser Ile Asn Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala			
	75	80	85
aga ttt tgg ata ttt aag gat caa aat aat agt cac caa aca aat aga			523
Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Ser His Gln Thr Asn Arg			
	90	95	100
ttt att tca tgg ttt aag gat aat ttg gct agc cca gga ggg tat gat			571
Phe Ile Ser Trp Phe Lys Asp Asn Leu Ala Ser Pro Gly Gly Tyr Asp			
	105	110	115
agt atc gct gaa cag atg ggc cta aaa gta gca gca tta aat gat atg			619
Ser Ile Ala Glu Gln Met Gly Leu Lys Val Ala Ala Leu Asn Asp Met			
	120	125	130
gat ata tca aat gta aat tat act tct aag aca ggg gat act ata tat			667
Asp Ile Ser Asn Val Asn Tyr Thr Ser Lys Thr Gly Asp Thr Ile Tyr			
	140	145	150
aat ggt gtt tca gaa tta aaa aat atc aca gga aca act caa aaa atg			715
Asn Gly Val Ser Glu Leu Lys Asn Ile Thr Gly Thr Thr Gln Lys Met			
	155	160	165
aaa aca gat agt ttt caa aga gat tat aca aaa tcc cag tca act tca			763
Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Gln Ser Thr Ser			
	170	175	180
atc acc aat gga tta caa tta gga ttt aaa gtt tca gct aaa gga ata			811
Ile Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ser Ala Lys Gly Ile			
	185	190	195
gtg gcc tta gcc ggt gcg gat ttt gaa gca agt gta aac tat aat tta			859
Val Ala Leu Ala Gly Ala Asp Phe Glu Ala Ser Val Asn Tyr Asn Leu			
	200	205	210
tcc act acc gca act gaa acc aat aca ata tct gat aaa ttt acc gtt			907
Ser Thr Thr Ala Thr Glu Thr Asn Thr Ile Ser Asp Lys Phe Thr Val			
	220	225	230
cct tca caa gaa gtc aca tta gcg cca gga cat aag gcg atc gta aaa			955
Pro Ser Gln Glu Val Thr Leu Ala Pro Gly His Lys Ala Ile Val Lys			
	235	240	245
cat agt ttg aag aaa atg gta tac tct gga acg cat gat tta aaa gga			1003
His Ser Leu Lys Lys Met Val Tyr Thr Ser Gly Thr His Asp Leu Lys Gly			
	250	255	260
gat tta aca att act ttt aat gat aag gat tta gtt caa aaa ttt att			1051
Asp Leu Thr Ile Thr Phe Asn Asp Lys Asp Leu Val Gln Lys Phe Ile			
	265	270	275
tat cca aat tat aaa gct att gat tta tct aat att cgt aaa gca atg			1099
Tyr Pro Asn Tyr Lys Ala Ile Asp Leu Ser Asn Ile Arg Lys Ala Met			
	280	285	290
aca gaa att gat gaa tgg aat cat gta aaa cct acc gat ttc tat caa			1147
Thr Glu Ile Asp Glu Trp Asn His Val Lys Pro Thr Asp Phe Tyr Gln			
	300	305	310

## 38-21(52806)B Sequence Listing.txt

tta gtt ggg aat aaa aat tat ata aaa aac ggg gac act tta tac atc 1195  
 Leu Val Gly Asn Lys Asn Tyr Ile Lys Asn Gly Asp Thr Leu Tyr Ile  
           315                                  320                                  325

gaa aca cct gct aaa ttc act ttg aat gga ggc aac cct tat tat aca 1243  
 Glu Thr Pro Ala Lys Phe Thr Leu Asn Gly Gly Asn Pro Tyr Tyr Thr  
           330                                  335                                  340

gca acc ttt acg gaa tat gat gaa aat gga aat caa gtc aaa aca aag 1291  
 Ala Thr Phe Thr Glu Tyr Asp Glu Asn Gly Asn Gln Val Lys Thr Lys  
           345                                  350                                  355

cgt tta aat aac aaa taagtactt aaaggtaatt cattaacaat gtatccatta 1346  
 Arg Leu Asn Asn Lys  
 360

tataattaat ttataaaaat aatgttttaa aa 1378

<210> 10

<211> 364

<212> PRT

<213> Bacillus thuringiensis

<400> 10

Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu  
 1                                  5                                  10                                  15

Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu  
           20                                  25                                  30

Thr Thr Ser Ser His Ala Val Thr Asn Gln Gln Thr Ile Thr Gln Arg  
           35                                  40                                  45

Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Gln Arg Asp  
           50                                  55                                  60

Ile Glu Ser Lys Met Thr Gly Lys Ser Ile Asn Met Gln Glu Gln Ile  
 65                                  70                                  75                                  80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
           85                                  90                                  95

Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu  
           100                                  105                                  110

Ala Ser Pro Gly Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys  
           115                                  120                                  125

Val Ala Ala Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser  
           130                                  135                                  140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile  
 145                                  150                                  155                                  160

Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
           165                                  170                                  175

38-21(52806)B Sequence Listing.txt

Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190

Lys Val Ser Ala Lys Gly Ile Val Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205

Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Thr  
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro  
225 230 235 240

Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser  
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys  
260 265 270

Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu  
275 280 285

Ser Asn Ile Arg Lys Ala Met Thr Glu Ile Asp Glu Trp Asn His Val  
290 295 300

Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys  
305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn  
325 330 335

Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Asn  
340 345 350

Gly Asn Gln Val Lys Thr Lys Arg Leu Asn Asn Lys  
355 360

<210> 11

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> probe sequence, or amplification primer sequence for use with primer as set forth in SEQ ID NO 12, corresponding to CDS as set forth in SEQ ID NO 3 from 438-458, biased toward codons preferred in Bacillus species genes containing A or T in 3rd position

<400> 11

aataataatc atcaaacwaa t

21

<210> 12

<211> 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> probe sequence, or amplification primer sequence for use with SEQ ID NO 11 corresponding to SEQ ID NO 3 from nucleotide position 978- 998, biased toward codons preferred in Bacillus species genes in which A or T is in 3rd position

&lt;400&gt; 12

attwggataw ataaattttt g

21

&lt;210&gt; 13

&lt;211&gt; 1101

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> coding sequence preferred for use in monocot species encoding a B t TIC901 amino acid sequence variant

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1101)

&lt;223&gt;

&lt;400&gt; 13

atg	aag	aac	cgc	ttc	agc	aag	gtc	gcc	ctc	tgc	acg	gtg	cct	atc	ctc	48
Met	Lys	Asn	Arg	Phe	Ser	Lys	Val	Ala	Leu	Cys	Thr	Val	Pro	Ile	Leu	
1			5						10					15		

atg	gtt	tct	acg	ttc	gcg	tcc	agc	tcg	atg	tcc	gcg	ttc	gca	gcg	gag	96
Met	Val	Ser	Thr	Phe	Ala	Ser	Ser	Ser	Met	Ser	Ala	Phe	Ala	Ala	Glu	
			20					25					30			

gcc	aaa	agt	cct	gac	ttg	aac	gtg	tcc	caa	cag	gtc	ata	ggc	cct	tac	144
Ala	Lys	Ser	Pro	Asp	Leu	Asn	Val	Ser	Gln	Gln	Val	Ile	Gly	Pro	Tyr	
		35				40						45				

gca	gaa	tct	tac	atc	gac	atc	gtc	cag	gac	aga	atg	aag	cag	aga	gac	192
Ala	Glu	Ser	Tyr	Ile	Asp	Ile	Val	Gln	Asp	Arg	Met	Lys	Gln	Arg	Asp	
	50					55					60					

aaa	gga	tcc	aaa	ctc	act	ggc	aaa	ccc	atc	aac	atg	caa	gag	cag	atc	240
Lys	Gly	Ser	Lys	Leu	Thr	Gly	Lys	Pro	Ile	Asn	Met	Gln	Glu	Gln	Ile	
65				70					75						80	

atc	gat	ggg	tgg	ttt	ctc	gca	cga	ttc	tgg	att	ttc	aag	gat	cag	aac	288
Ile	Asp	Gly	Trp	Phe	Leu	Ala	Arg	Phe	Trp	Ile	Phe	Lys	Asp	Gln	Asn	
			85					90						95		

aat	aac	cac	cag	aca	aac	agg	ttc	atc	tca	tgg	ttt	aag	gat	aac	atc	336
Asn	Asn	His	Gln	Thr	Asn	Arg	Phe	Ile	Ser	Trp	Phe	Lys	Asp	Asn	Ile	
			100				105						110			

gcc	tca	tct	aag	gga	tac	aac	tca	ata	gcc	gaa	cag	atg	ggc	ctc	aaa	384
Ala	Ser	Ser	Lys	Gly	Tyr	Asn	Ser	Ile	Ala	Glu	Gln	Met	Gly	Leu	Lys	
		115				120						125				

## 38-21(52806)B Sequence Listing.txt

```

atc gaa gca gag aat gat atg gac gtg aca aat atc gac tac act agt      432
Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser
   130                               135                               140

aag acc gga gac aca atc tac aac ggc att tcg gaa ctt aaa aac tat      480
Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr
   145                               150                               155                               160

acg ggc agc acc cag aaa atg aag acc gat agc ttt caa agg gac tac      528
Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
                               165                               170                               175

aca aaa tcc gag tcg acc tcc gtg acc aat ggc ctc cag ctg ggc ttc      576
Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe
                               180                               185                               190

aag gtg gca gca aag ggc gtc gtc gct tta gcc ggc gca gac ttc gag      624
Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu
                               195                               200                               205

act tcg gtg acc tac aat ctg tct aca act acg act gag acg aac aca      672
Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr
   210                               215                               220

att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc cct cca      720
Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro
   225                               230                               235                               240

ggc cac aag gca atc gtc aag cac gac ctg agg aaa atg gtc tac agc      768
Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser
                               245                               250                               255

ggc acc cat gat ctc aaa ggc gac ctc atc gtg tcg ttc aac gac aag      816
Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys
                               260                               265                               270

gag ata gtc cag aag ttc atc tac cca aat tac cgc gac atc aac ctc      864
Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Asp Ile Asn Leu
   275                               280                               285

agt gac atc cga gag acc atg atc gag atc gac gag tgg aac cac gtg      912
Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val
   290                               295                               300

aac cct gtc aat ttc tac gaa ctc gta gga gtt aag aac cac atc aag      960
Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys
   305                               310                               315                               320

aac ggt gaa aca ttg tac atc gac acg ccg gct aag ttc atg ttc aac     1008
Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn
                               325                               330                               335

gga gcg aat cct tac tat cga gct acc ttc acg gag tac gat ggc aac     1056
Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn
                               340                               345                               350

aac aat cct gtt cag acc aag gtg ttg agt gag aat ttc aag ctg         1101
Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu
   355                               360                               365

```

&lt;210&gt; 14

&lt;211&gt; 367

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;



<223> coding sequence preferred for use in monocot species encoding a B  
t TIC901 amino acid sequence variant

<400> 14

Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu  
1 5 10 15

Met Val Ser Thr Phe Ala Ser Ser Ser Met Ser Ala Phe Ala Ala Glu  
20 25 30

Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr  
35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp  
50 55 60

Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile  
100 105 110

Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys  
115 120 125

Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser  
130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr  
145 150 155 160

Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr  
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro  
225 230 235 240

Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser  
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys  
260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Asp Ile Asn Leu  
Page 17

275

280

Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val  
290 295 300

Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys  
305 310 315 320

Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn  
325 330 335

Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn  
340 345 350

Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu  
355 360 365

<210> 15

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW152 SEQ ID NO 16 in thermal amplification reactions

<400> 15  
cctttggcag aaactttaac tcc 23

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW151 SEQ ID NO 15 in thermal amplification reactions

<400> 16  
gtgtattctg gtacgcatga c 21

<210> 17

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW183 SEQ ID NO 18 in thermal amplification reactions

## mal amplification reactions

<400> 17  
gccggatccc tagctgaata tgcagtagat aatg 34

<210> 18

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW186 SEQ ID NO 17 in thermal amplification reactions

<400> 18  
gtggcacggtt tataggccat tgttc 25

<210> 19

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW156 SEQ ID NO 20 in thermal amplification reactions

<400> 19  
cttttaggcc catctgttca gcg 23

<210> 20

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW155 SEQ ID NO 19 in thermal amplification reactions

<400> 20  
gccttagccg gtgcggattt tgaagc 26

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

38-21(52806)B Sequence Listing.txt

<223> oligonucleotide primer coupled with prJPW170 SEQ ID NO 22 in thermal amplification reactions

<400> 21  
ggagcttatt tgttatttaa acgctttggt ttgacttgat ttcc 44

<210> 22

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW168 SEQ ID NO 21 in thermal amplification reactions

<400> 22  
gccggatccc agtggatagg aatttgtttt cgtgctagg 39

<210> 23

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:24 and SEQ ID NO:25 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 23  
aayatgcarg arcarathat hgaygg 26

<210> 24

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:23 and SEQ ID NO:25 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 24  
aayatgcarg arcarathat hga 23

<210> 25

<211> 20

38-21(52806)B Sequence Listing.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:23 and SEQ ID NO:24 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 25

aayatgcarg arcarathat

20

<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, 431 and the like result in amplicon of from about 395 to about 425 base pairs

<220>

<221> misc\_feature

<222> (3)..(3)

<223> inosine

<220>

<221> misc\_feature

<222> (9)..(9)

<223> inosine

<400> 26

ggngayacna thtayaaygg

20

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> universal reverse amplification primer similar to SEQ ID NO:28 and SEQ ID NO:29

38-21(52806)B Sequence Listing.txt

<220>

<221> misc\_feature

<222> (6)..(6)

<223> inosine

<220>

<221> misc\_feature

<222> (24)..(24)

<223> inosine

<400> 27

tarttnggrt adatraaytt ytgnac

26

<210> 28

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> universal reverse amplification primer similar to SEQ ID NO:27 and SEQ ID NO:29

<220>

<221> misc\_feature

<222> (6)..(6)

<223> inosine

<400> 28

tarttnggrt adatraaytt ytg

23

<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> universal reverse amplification primer similar to SEQ ID NO:27 and SEQ ID NO:28

<220>

<221> misc\_feature

<222> (18)..(18)

38-21(52806)B Sequence Listing.txt

<223> inosine

<400> 29  
ggrtadatra ayttytgnac 20

<210> 30

<211> 570

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (1)..(570)

<223>

<400> 30  
ttt tta gct aga ttt tgg ata ttt gag gat caa aat aat agt cac caa 48  
Phe Leu Ala Arg Phe Trp Ile Phe Glu Asp Gln Asn Asn Ser His Gln  
1 5 10 15  
aca aat aga ttt att tca tgg ttt aag gat aat att gct agt tca aaa 96  
Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile Ala Ser Ser Lys  
20 25 30  
ggg tat aat agt att gcg gag caa atg ggt tta aaa ata gaa gca gaa 144  
Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala Glu  
35 40 45  
aac gat atg gat gta aca aat ata gat tat aca tct aag aca ggc gat 192  
Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp  
50 55 60  
acc att tat aat ggt att tca gaa ttg aaa aat tat aca gga tca act 240  
Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr Thr Gly Ser Thr  
65 70 75 80  
caa aag atg aaa aca gat agt ttt caa aga gat tat aca aaa tca gaa 288  
Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Glu  
85 90 95  
tct act tca gta act aat gga tta caa tta gga ttt aaa gtt gct gct 336  
Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala Ala  
100 105 110  
aaa gga gta gtt gct ttg gct ggg gca gac ttt gaa acc agt gtt act 384  
Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val Thr  
115 120 125  
tat aat cta tca act act aca act gaa aca aat aca ata tca gac aag 432  
Tyr Asn Leu Ser Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp Lys  
130 135 140  
ttt act gtc cca tct caa gaa gtt aca ttg cct cca gga cat aaa gcg 480  
Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys Ala  
145 150 155 160  
ata gtg aaa cat gat tta aga aaa atg gtt tat tct ggt act cat gat 528  
Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp  
165 170 175

## 38-21(52806)B Sequence Listing.txt

cta aag ggt gat tta att gtg agt ttt aat gat aaa gag att 570  
 Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys Glu Ile  
           180                  185                  190

<210> 31

<211> 190

<212> PRT

<213> Bacillus thuringiensis

<400> 31

Phe Leu Ala Arg Phe Trp Ile Phe Glu Asp Gln Asn Asn Ser His Gln  
   1                  5                  10                  15

Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile Ala Ser Ser Lys  
           20                  25                  30

Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala Glu  
           35                  40                  45

Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp  
           50                  55                  60

Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr Thr Gly Ser Thr  
   65                  70                  75                  80

Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Glu  
           85                  90                  95

Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala Ala  
           100                  105                  110

Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val Thr  
           115                  120                  125

Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp Lys  
           130                  135                  140

Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys Ala  
   145                  150                  155                  160

Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp  
           165                  170                  175

Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys Glu Ile  
           180                  185                  190

<210> 32

<211> 1095

<212> DNA

<213> Bacillus thuringiensis



38-21(52806)B Sequence Listing.txt

<220>

<221> CDS

<222> (1)..(1092)

<223> sequence encoding TIC431 precursor amino acid sequence

<400> 32

atg aaa tac aag tct tca aaa gta gca atg tgt aca tta tcg gct tta	48
Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu	
1 5 10 15	
atg ctt tcg aca atc gcc act cca agt ata tct gtt ttc gct gct gaa	96
Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu	
20 25 30	
aca act gca tca cat aag gtt act aat cag caa aca att gca cag cgt	144
Thr Thr Ala Ser His Lys Val Asn Gln Gln Thr Ile Ala Gln Arg	
35 40 45	
gca gaa tct tat atc gat att gtg cat aat aga atg aaa aaa cga gat	192
Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Lys Arg Asp	
50 55 60	
att gaa tca aaa atg aca ggt aaa cct att aat atg caa gaa caa ata	240
Ile Glu Ser Lys Met Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile	
65 70 75 80	
att gat gga tgg ttt tta gct aga ttt tgg ata ttc aag gac caa aat	288
Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn	
85 90 95	
aat agt cac caa aca aat aga ttt att tca tgg ttt aaa gat aat tta	336
Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu	
100 105 110	
gct agt cca gga ggg tat aat agt atc gct aaa caa atg ggg tta aaa	384
Ala Ser Pro Gly Gly Tyr Asn Ser Ile Ala Lys Gln Met Gly Leu Lys	
115 120 125	
ata gaa gta tta aat gat atg gat ata tca aat gta aat tat act tct	432
Ile Glu Val Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser	
130 135 140	
aag aca ggg gat act ata tat aat ggt gtt tcc gaa tta aaa aat atc	480
Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile	
145 150 155 160	
aca ggt aca act caa aaa atg aaa aca gat agt ttt caa aga gat tat	528
Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr	
165 170 175	
aca aaa tca cag tca act tca atc acc aat gga tta caa tta gga ttt	576
Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe	
180 185 190	
aaa gtt tct gcc aaa ggg gtg ata gct tta gca gga gca gac ttc gaa	624
Lys Val Ser Ala Lys Gly Val Ile Ala Leu Ala Gly Ala Asp Phe Glu	
195 200 205	
gca agt gtc aac tat aat tta tcc act acc gca act gaa acc aat ata	672
Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Ile	
210 215 220	
ata tct gat aaa ttt acc gtt cct tca caa gaa gtt aca tta gcg cca	720
Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro	
225 230 235 240	
gga cat aag gcg atc gta aaa cat agt tta aag aaa atg gta tac tcc	768
Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser	

## 38-21(52806)B Sequence Listing.txt

245	250	255	
gga acg cat gat tta aaa gga gat tta aca att act ttt aat gat aag	816		
Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys			
260 265 270			
gat tta gtt caa aaa ttt att tat cca aat tat aaa gct att gat tta	864		
Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu			
275 280 285			
tct aat att cgt aaa gca ctg act gaa att gat gaa tgg aat cat gta	912		
Ser Asn Ile Arg Lys Ala Leu Thr Glu Ile Asp Glu Trp Asn His Val			
290 295 300			
aaa cct acc gat ttc tat caa tta gtt ggg aac aaa aat tat ata aaa	960		
Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys			
305 310 315 320			
aac ggg gac act tta tac atc gaa aca cct gct aaa ttc act ttg aat	1008		
Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn			
325 330 335			
gga gga aac cct tat tat aca gca acc ttt acg gaa tat gat gaa agt	1056		
Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Ser			
340 345 350			
gga aat caa gtc aaa aca aag cat tta agt gtc aaa taa	1095		
Gly Asn Gln Val Lys Thr Lys His Leu Ser Val Lys			
355 360			

&lt;210&gt; 33

&lt;211&gt; 364

&lt;212&gt; PRT

&lt;213&gt; Bacillus thuringiensis

&lt;400&gt; 33

Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu
1 5 10 15

Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu
20 25 30

Thr Thr Ala Ser His Lys Val Thr Asn Gln Gln Thr Ile Ala Gln Arg
35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Lys Arg Asp
50 55 60

Ile Glu Ser Lys Met Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
85 90 95

Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu
100 105 110

Ala Ser Pro Gly Gly Tyr Asn Ser Ile Ala Lys Gln Met Gly Leu Lys
115 120 125

38-21(52806)B Sequence Listing.txt

Ile Glu Val Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser  
130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile  
145 150 155 160

Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
165 170 175

Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190

Lys Val Ser Ala Lys Gly Val Ile Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205

Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Ile  
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro  
225 230 235 240

Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser  
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys  
260 265 270

Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu  
275 280 285

Ser Asn Ile Arg Lys Ala Leu Thr Glu Ile Asp Glu Trp Asn His Val  
290 295 300

Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys  
305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn  
325 330 335

Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Ser  
340 345 350

Gly Asn Gln Val Lys Thr Lys His Leu Ser Val Lys  
355 360